## A General and Parallel Platform for Mining Co-Movement Patterns over Large-scale Trajectories

#### **ABSTRACT**

#### 1. INTRODUCTION

The prevalence of positioning devices has drastically boosted the scale and spectrum of trajectory collection to an unprecedented level. Tremendous amounts of trajectories, in the form of sequenced spatial-temporal records, are continually generated from animal telemetry chips, vehicle GPSs and wearable devices. Data analysis on large-scale trajectories benefits a wide range of applications and services, including traffic planning [1], animal analysis [2], and social recommendations [3], to name just a few.

A crucial task of data analysis on top of trajectories is to discover co-moving patterns. A co-movement pattern [4] refers to a group of objects traveling together for a certain period of time and the group is normally determined by spatial proximity. A pattern is prominent if the size of the group exceeds M and the length of the duration exceeds K, where M and K are parameters specified by users. Rooted from such basic definition and driven by different mining applications, there are a bunch of variants of co-movement patterns that have been developed with more advanced constraints.

Table 1 summarizes several popular co-moving pattern s with different constraints in the attributes of clustering in spatial proximity, consecutiveness in temporal duration and computational complexity. In particular, the flock [5] and the group [6] patterns require all the objects in a group to be enclosed by a disk with radius r; whereas the convoy [7], the swarm [8] and the platoon [9] patterns resort to densitybased spatial clustering. In the temporal dimension, the flock [5] and the convoy [7] require all the timestamps of each detected spatial group to be consecutive, which is referred to as global consecutiveness; whereas the swarm [8] does not impose any restriction. The group [6] and the platoon [9] adopt a compromised manner by allowing arbitrary gaps between the consecutive segments, which is called local consecutiveness. They introduce a parameter L to control the minimum length of each local consecutive segment.

ſ	Patterns	Proximity	Consecutiveness	Time Complexity
ſ	flock [10]	disk-based	global	$O( \mathbb{O}  \mathbb{T} (M + log( \mathbb{O} ))$
	convoy [7]	density-based	global	$O( \mathbb{O} ^2 +  \mathbb{O}  \mathbb{T} )$
ſ	swarm [8]	density-based	-	$O(2^{ \mathbb{O} } \mathbb{O}  \mathbb{T} )$
ſ	group [6]	disk-based	local	$O( \mathbb{O} ^2 \mathbb{T} )$
	platoon [9]	density-based	local	$O(2^{ \mathbb{O} } \mathbb{O}  \mathbb{T} )$

Table 1: Constraints and complexity of co-movement patterns. The time complexity indicates the performance in the worst case, where  $|\mathbb{O}|$  is the total number of objects and  $|\mathbb{T}|$  is the number of descritized timestamps.

Figure 1 is an example to demonstrate the concepts of various co-movement patterns. The trajectory database consists of six moving objects and the temporal dimension is discretized into six snapshots. In each snapshot, we treat the clustering methods as a black-box and assume that they generate the same clusters. Objects in proximity are grouped in the dotted circles. As aforementioned, there are three parameters to determine the co-movement patterns and the default settings in this example are M=2, K=3 and L=2. Both the *flock* and the *convoy* require the spatial clusters to last for at least K consecutive timestamps. Hence,  $\{o_3, o_4\}$ and  $\{o_5, o_6\}$  remains the only two candidates matching the patterns. The swarm relaxes the pattern matching by discarding the temporal consecutiveness constraint. Thus, it generates many more candidates than the flock and the convoy. The group and the platoon add another constraint on local consecutiveness to retain meaningful patterns. For instance,  $\{o_1, o_2 : 1, 2, 4, 5\}$  is a pattern matching local consecutiveness because timestamps  $\{1,2\}$  and  $\{4,5\}$  are two segments with length no smaller than L=2. The difference between the group and the platoon is that the platoon has an additional parameter K to specify the minimum number of snapshots for the spatial clusters. This explains why  $\{o_3, o_4, o_5 : 2, 3\}$  is a group pattern but not a platoon pat-

As can be seen, there are various co-movement patterns requested by different applications and it is cumbersome to design a tailored solution for each type. In addition, despite the generality of the platoon (i.e., it can be reduced to other types of patterns via proper parameter settings), it suffers from the so-called loose-connection anomaly. We use two objects  $o_1$  and  $o_2$  in Figure 2 as an example to illustrate the scenario. These two objects form a platoon pattern in timestamps  $\{1, 2, 3, 102, 103, 104\}$ . However, the two consecutive segments are 98 timestamps apart, resulting in a false positive co-movement pattern. In reality, such an anomaly may be caused by the periodic movements of unrelated ob-

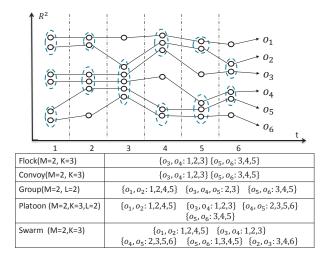


Figure 1: Trajectories and co-movement patterns; The example consists of six trajectories across six snapshots. Objects in spatial clusters are enclosed by dotted circles. M is the minimum cluster cardinality; K denotes the minimum number of snapshots for the occurrence of a spatial cluster; and L denotes the minimum length for local consecutiveness.

jects, such as vehicles stopping at the same petrol station or animals pausing at the same water source. Unfortunately, none of the existing patterns have directly addressed this anomaly.

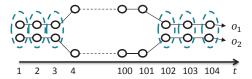


Figure 2: Loose-connection anomaly. Even though  $\{o_1, o_2 : 1, 2, 3, 102, 103, 104\}$  is considered as a valid platoon pattern, it is highly probable that these two objects are not related as the two consecutive segments are 98 timestamps apart.

The other issue with existing methods is that they are built on top of centralized indexes which may not be scalable. Table 1 shows their theoretical complexities in the worst cases and the largest real dataset ever evaluated in previous studies is up to million-scale points collected from hundreds of moving objects. In practice, the dataset is of much higher scale and the scalability of existing methods is left unknown. Thus, we conduct an experimental evaluation with 4000 objects moving for 2500 timestamps to examine the scalability. Results in Figure 3 show that their performances degrade dramatically as the dataset scales up. For instance, the detection time of group drops twenty times as the number of objects grows from 1k to 4k. Similarly, the performance of swarm drops over fifteen times as the number of snapshots grows from 1k to 2.5k. These observations imply that existing methods are not scalable to support large-scale trajectory databases.

Therefore, our primary contributions in this paper are to close these two gaps. First, we propose the *general co-movement pattern* (GCMP) which models various co-moment patterns in a unified way and can avoid the *loose-connection* 

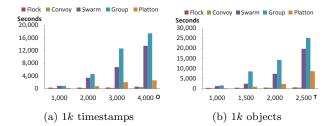


Figure 3: Performance measures on existing co-movement patterns. A sampled Geolife data set is used with up two 2.4 million data points. Default parameters are M=15 K=180 L=30.

anomaly. In GCMP, we introduce a new gap parameter G to pose a constraint on the temporal gap between two consecutive segments. By setting a feasible G, the loose-connection anomaly can be avoided. In addition, our GCMP is both general and expressive. It can be reduced to any of the previous patterns by customizing the parameters.

Second, we investigate deploying our GCMP detector on MapReduce platforms (such as Hadoop and Spark) to tackle the scalability issue. Our technical contributions are threefold. First, we replicate the snapshots in multiple data chunks to support efficient parallel processing. Second, we devise a novel Star Partition and ApRiori Enumerator (SPARE) framework as a fine-granularity partitioning strategy to achieve workload balance. For each star, an Apriori Enumerator is adopted to mine the co-movement patterns. Third, we leverage the temporal monotonicity property of GCMP to design several optimization techniques including sequence simplification, monontonicity pruning and forward closure check to further reduce the number of candidates enumerated.

We conduct a set of extensive experiments on three large-scaled real datasets with hundreds of millions temporal points. The results show that both our parallel scheme efficiently supports GCMP mining in large datasets. In particular, with near 200 million trajectory points, SPARE runs in 15 minutes using 162 cores. Whereas centralized solutions take near 7 hours for 1 million trajectory points. Moreover, our optimized SPARE methods achieves upto 10 times efficiency as compared to the baseline algorithm with almost linear scalability.

The rest of our paper is organized as follows: Section 2 summarizes the relevant literature on trajectory pattern mining. Section 3 states the problem definition of our general co-movement pattern mining. Section 4 provides a baseline solution. An advanced solution named star partition and mining is presented in Section 5. Section 6 conducts extensive experiments to verify the efficiency of our system. Finally Section 7 concludes the paper.

#### 2. RELATED WORKS

The co-movement patterns in literature consist of five members, namely group [6], flock [10], convoy [7], swarm [8] and platoon [9]. We have demonstrated the semantics of these patterns in Table 1 and Figure 1. In this section, we focus on comparing the techniques used in these works. For more trajectory patterns other than co-movement patterns, interested readers may move to [11] for a comprehensive survey.

## 2.1 Flock and Convoy

The difference between flock and convoy lies in the object clustering methods. In flock objects are clustered based on their distance. Specifically, the objects in the same cluster needs to have a pair-wised distance less than min\_dist. This essentially requires the objects to be within a disk-region of delimiter less than min\_dist. In contrast, convoy cluster the objects using density-based clustering [12]. Technically, flock utilizes a  $m^{th}$ -order Voronoi diagram [13] to detect whether a subset of object with size greater than m stays in a disk-region. Convoy employs a trajectory simplification [14] technique to boost pairwise distance computations in the density-based clustering. After clustering, both flock and *convoy* use a line-sweep method to scan each snapshots. During the scan, the object group appears in consecutive timestamps is detected. Meanwhile, the object groups that do not match the consecutive constraint are pruned. However, such a method faces high complexity issues when supporting other patterns. For instance, in swarm, the candidate set during the line-sweep grows exponentially, and many candidates can only be pruned after the entire snapshots are scanned.

## 2.2 Group, Swarm and Platoon

Different from flock and convoy, all the group, swarm and platoon patterns have more constraints on the pattern duration. Therefore, their techniques of mining are of the same skeleton. The main idea of mining is to grow object set from an empty set in a depth-first manner. During the growth, various pruning techniques are provided to prune unnecessary branches. Group pattern uses the Apriori property among patterns to facilitate the pruning. Swarm adapts two more pruning rules called backward pruning and forward pruning. Platoon further adapts a prefix table structure to guide the depth-first search. As shown by Li et.al. [9], platoon outperforms other two methods in efficiency. However, the three patterns are not able to directly discover the general co-movement pattern. Furthermore, their pruning rules heavily rely on the depth-first search nature, which lost its efficiency in the parallel scenario.

#### 3. **DEFINITIONS**

Let  $\mathbb{O}=\{o_1,o_2,...,o_n\}$  be the set of objects and  $\mathbb{T}=(1,2,...,N)$  be the discretized temporal dimension. A time sequence T is defined as a ordered subset of  $\mathbb{T}$ . Given two time sequences  $T_1$  and  $T_2$ , we define a bunch of commonly-used operators in this paper in Table 2.

Operator	Definition	
T[i]	the $i$ -th element in the sequence $T$	
T	the number of elements in T	
$\max(T)$	the maximum element in T	
$\min(T)$	the minimum element in $T$	
range(T)	the range of T, i.e., $max(T) - min(T) + 1$	
T[i:j]	subsequence of $T$ from $T[i]$ to $T[j]$ (inclusive)	
$T_1 \subseteq T_2$	$\forall T_1[x] \in T_1$ , we have $T_1[x] \in T_2$ .	
$T_3 = T_1 \cup T_2$	$\forall T_3[x] \in T_3$ , we have $T_3[x] \in T_1$ or $T_3[x] \in T_2$	
$T_3 = T_1 \cap T_2$	$\forall T_3[x] \in T_3$ , we have $T_3[x] \in T_1$ and $T_3[x] \in T_2$	

Table 2: Operators on time sequence.

We say a sequence T is consecutive if  $\forall i \in (1, ..., |T| - 1), T[i+1] = T[i]+1$ . We refer each consecutive subsequence of T as a *segment*. It is obvious that any time sequence

T can be decomposed into segments and we say T is L-consecutive [9] if the length of every segment is no smaller than L. As illustrated in Figure 2, patterns adopting the notion of L-consecutiveness (e.g., platoon and group) still suffer from the loose connection problem. To avoid such an anomaly without losing pattern generality, we introduce a parameter G to control the gaps between timestamps in a pattern. Formally, a G-connected time sequence is defined as follows:

**Definition 1** (G-connected). A time sequence T is G-connected if the gap between any of its neighboring timestamps is no greater than G. That is  $\forall i \in (1,...,|T|-1), T[i+1]-T[i] \leq G$ .

We take T = (1, 2, 3, 5, 6) as an example, which can be decomposed into two segments (1, 2, 3) and (5, 6). T is not 3-consecutive since the length of (5, 6) is 2. Thus, it is safe to say either T is 1-consecutive or 2-consecutive. On the other hand, T is 2-connected since the maximum gap between its neighboring time stamps is 5-3=2. It is worth noting that T is not 1-connected because the gap between T[3] and T[4] is 2 (i.e., 5-3=2).

Given a trajectory database discretized into snapshots, we can conduct a clustering method, either disk-based or density-based, to identify groups with spatial proximity. Let T be the set of timestamps in which a group of objects O are clustered. We are ready to define a more general comovement pattern:

**Definition 2** (General Co-Movement Pattern). A general co-movement pattern finds a set of objects O satisfying the following five constraints: (1) closeness: the objects in O belong to the same cluster in the timestamps of T; (2) significance:  $|O| \geq M$ ; (3) duration:  $|T| \geq K$ ; (4) consecutiveness: T is L-consecutive; and (5) connection: T is G-connected.

There are four parameters in our general co-movement pattern, including object constraint M and temporal constraints K, L, G. By customizing these parameters, our pattern can express other patterns proposed in previous literature, as illustrated in Table 3. In particular, by setting  $G = |\mathbb{T}|$ , we achieve the *platoon* pattern. By setting  $G = |\mathbb{T}|$ , M = 2, K = 1, we gain the *group* pattern. Finally by setting G = 1, we achieve the *convoy* and *flock* patterns. In addition to the flexibility of representing other existing patterns, our GCMP is able to avoid the *loose connection* anomaly by tuning the parameter G. It is notable that GCMP cannot be modeled by existing patterns.

Pattern	M	K	L	G	Clustering
Group	2	1	2	$ \mathbb{T} $	Disk-based
Flock			K	1	Disk-based
Convoy			K	1	Density-based
Swarm			1	$ \mathbb{T} $	Density-based
Platoon				$ \mathbb{T} $	Density-based

Table 3: Expressing other patterns using GCMP.  $\cdot$  indicates a user specified value. M represents the object size constraint. K represents the duration constraint. L represents the consecutiveness constraint. G represents the connection constraint.

Our definition of GCMP is independent of the clustering method. Users can apply different clustering methods to facilitate different application needs. We currently expose both disc-region based clustering and DBSCAN as options to the users. In summary, the goal of this paper is to present a parallel solution for discovering all the valid GCMP from large-scale trajectory datasets. Before we move on to the algorithmic part, we list the notations that are used in the following sections.

Symbol	Meaning	
$S_t$	snapshot of objects at time t	
M	object size constraint	
K	duration constraint	
L	consecutiveness constraint	
G	connection constraint	
$P = \langle O : T \rangle$	pattern with object set $O$ , time sequence $T$	
η	replication factor in the TRPM framework	
$C_t(o)$	the cluster of object $o$ at time $t$	
$S_t$	the set of clusters at time $t$	
$\lambda_t$	$\lambda_t$ the partition with snapshots $S_t,, S_{t+\eta-1}$	
$Sr_i$	the star partition for object $i$	

Table 4: Symbols and notions used

# 4. BASELINE: TEMPORAL REPLICATION AND PARALLEL MINING

In this section, we propose a baseline solution that resorts to MapReduce (MR) as a general, parallel and scalable paradigm for GCMP pattern mining. The framework, named temporal replication and parallel mining (TRPM), is illustrated in Figure 4. There are two cycles of mapreduce jobs connected in a pipeline manner. The first cycle deals with spatial clustering in each snapshot, which can be seen as a preprocessing step for the subsequent pattern mining. In particular, the timestamp is treated as the key in the map phase and objects within the same snapshot are clustered (DBSCAN or disk-based clustering) in the reduce phase. Finally, the reducers output clusters of objects in each snapshot, represented by a list of  $\langle t, S_t \rangle$  pairs, where t is the timestamp and  $S_t$  is a set of clustered objects at snapshot t.

Our focus in this paper is the second map-reduce cycle of parallel mining, which essentially consists of two key questions to solve. The first is how to employ effective data partitioning such that the mining can be conducted independently; and the second is how to efficiently mine the valid patterns within each partition.

It is obvious that we cannot simply split the trajectory database into disjoint partitions because a GCMP pattern requires L-consecutiveness and the corresponding segments may cross multiple partitions. Our strategy is to use data replication to enable parallel mining. Each snapshot will replicate its clusters to  $\eta-1$  preceding snapshots. In other words, the partition for the snapshot  $S_t$  contains clusters in  $S_t, S_{t+1} \ldots, S_{t+\eta-1}$ . Determining a proper  $\eta$  is critical in ensuring the correctness and efficiency of TRPM. If  $\eta$  is too small, certain cross-partition patterns may be missed. If  $\eta$  is set too large, expensive network communication and CPU processing costs would be incurred in the map and reduce phases respectively. Our objective is to find an  $\eta$  that is not large but can guarantee correctness.

In our implementation, we set  $\eta = (\lceil \frac{K}{L} \rceil - 1) * (G-1) + K + L - 1$ . Intuitively, K timestamps generates at most  $\lceil \frac{K}{L} \rceil - 1$ 

gaps as the length of each L-consecutive segment is at least L. Since the gap size is at most G-1,  $(\lceil \frac{K}{L} \rceil - 1) * (G-1)$  is the upper bound of timestamps allocated to gaps. The remaining part K+L-1 is used to capture the upper bound allocated for the L-consecutive segments. We formally prove that  $\eta$  can guarantee correctness.

**Theorem 1.**  $\eta = (\lceil \frac{K}{L} \rceil - 1) * (G - 1) + K + L - 1$  guarantees that no valid pattern is missing.

*Proof.* Given a valid pattern P, we can always find at least one valid subsequence that is also valid. Let T' denote the valid subsequence with the minimum length. In the worst case, T' = P.T. We define range $(T) = \max(T) - \min(T) + 1$ and prove the theorem by showing that range(T')  $\leq \eta$ . Since T' can be written as a sequence of L-consecutive segments interleaved by gaps:  $l_1, g_1, \ldots, l_{n-1}, g_{n-1}, l_n \ (n \ge 1)$ , where  $l_i$  is a segment and  $g_i$  is a gap. Then, range(T') is calculated as  $\sum_{i=1}^{i=n}|l_i|+\sum_{i=1}^{i=n-1}|g_i|$ . Since T' is valid, then  $\sum_{i=1}^{i=n}|l_i|\geq K$ . As T' is minimum, if we remove the last  $l_n$ , the resulting sequence should not be valid. Let  $K' = \sum_{i=1}^{i=n-1} |l_i|$ , which is the size of the first (n-1) segments of T'. Then,  $K' \leq K-1$ . Note that every  $|l_i| \geq L$ , thus  $n \leq \lceil \frac{K'}{L} \rceil \leq \lceil \frac{K}{L} \rceil$ . By using the fact that every  $|g_i| \leq G - 1$ , we achieve  $\sum_{i=1}^{i=n-1} |g_i| \leq (n-1)(G-1) \leq (\lceil \frac{K}{L} \rceil - 1)(G-1)$ . Next, we consider the difference between K and K', denoted by  $\Delta = K - K'$ . K'. To ensure T''s validity,  $l_n$  must equal to  $\min(L, \Delta)$ . Then,  $\sum_{i=1}^{i=n} |l_i| = K' + l_n = K - \Delta + \min(L, \Delta) \le K - 1 + M$ L. We finish showing range $(T') \leq \eta$ . Therefore, for any valid sequence T, it exists at least one valid subsequence with range no greater than  $\eta$  and hence this pattern can be detected in a partition with  $\eta$  snapshots.

Based on the above theorem, during TRPM, every consecutive  $\eta$  snapshots form a partition. In other words, each snapshot  $S_t$  corresponds to a partition  $\lambda_t = \{S_t, ..., S_{t+\eta-1}\}$ . Our next task is to design an efficient pattern mining strategy within each partition. We propose a line sweep algorithm to sequentially scan the  $\eta$  replicated snapshots in a partition and employ effective candidate pattern enumeration.

Details of the algorithm are presented in Algorithm 1. We keep a candidate set C (Line 1) during the sweeping process. It is initialized as the candidate clusters with size no smaller than M in the first snapshot. Then, we sequentially scan each snapshot (Lines 7-27) and generate new candidates by extending the original ones in C. In particular, we join candidates in C with all the clusters in  $S_i$  to form new candidates (Lines 9-16). After sweeping all the snapshots, all the valid patterns are stored in C(Line 28). It is worth noting that C continues to grow during the whole sweeping process. We can use three pruning rules to early remove false candidates from C. Since there is a partition  $\lambda_t$  for each  $S_t$ , in line sweep, only patterns that starts from timestamp t (i.e.,  $S_t$ ) need to be discovered. Therefore, those patterns that does not appear in the  $S_t$  are false candidates. Particularly, our three pruning rules are as follows: First, when sweeping snapshot  $S_i$ , new candidates with objects set smaller than M are pruned (Line 14). Second, after joined with all clusters in  $S_i$ , candidates in C with the maximum timestamp no greater than j-G are pruned (Lines 18-21). Third, candidates in C with the size of first segment smaller than Lare pruned (Lines 22-24). With the three pruning rules, the size of C could be significantly reduced.

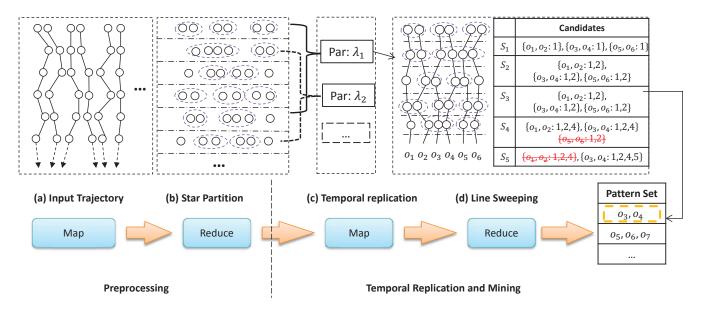


Figure 4: Work flow of Temporal Replication and Parallel Mining. (a)(b) correspond to the first map-reduce cycle which clusters objects in each snapshot; (c)(d) correspond to the second map-reduce cycle uses TRPM to detect GCMP in parallel.

The complete picture of temporal replication and parallel mining is summarized in Algorithm 2. We illustrate the workflow of TRPM method using Figure 4 (c)(d) with pattern parameters M=2, K=3, L=2, G=2. By Theorem 1,  $\eta$  is calculated as  $(\lceil \frac{K}{L} \rceil - 1) * (G - 1) + 2K - 2 = 5$ . Therefore, in Figure 4 (c), every 5 consecutive snapshots are combined into a partition in the map phase. In Figure 4 (d), a line sweep method is illustrated for partition  $\lambda_1$ . Let  $C_i$  be the candidate set during sweeping snapshot  $S_i$ . Initially,  $C_1$  contains patterns with object sets in snapshot  $S_1$ . As we sweep the snapshots, the patterns in  $C_i$ grow. At snapshot  $S_4$ , the candidate  $\{o_5, o_6\}$  is removed. This is because the gap between its latest timestamp (i.e., 2) and the next scanning timestamp (i.e., 5) is 3, which violates the G-connected constraint. Next, at snapshot  $S_5$ , the candidate  $\{o_1, o_2\}$  is removed. This is because its local consecutive segment {4} has only 1 element, which violates the L-consecutive constraint. Finally,  $\{o_3, o_4\}$  is the valid pattern and is returned. Note that in this example,  $\eta = 5$  is the minimum setting that can guarantee correctness. If  $\eta$  is set to 4, the pattern  $\{o_3, o_4\}$  would be missed.

## 5. SPARE: STAR PARTITIONING AND APRI-ORI ENUMERATOR

The aforementioned replicate partitioning is based on the temporal dimension which suffers from two drawbacks. First, the replication relies on  $\eta$  which could be large. Second, the same valid pattern may be discovered from different partitions which results in redundant works. To resolve the limitations caused by the replicate partitioning, we propose a new Star Partitioning and ApRiori Enumerator, named SPARE, to replace the second cycle of map-reduce jobs in Figure 4. Our new parallel mining framework is shown in Figure 5. Its input is the set of clusters generated in each snapshot and the output contains all the valid GCMP pat-

terns. In the following, we explain the two major components: star partitioning and apriori enumerator.

## 5.1 Star Partitioning

Let  $G_t$  be a graph for snapshot  $S_t$ , in which each node is a moving object and two objects are connected if they appear in the same cluster. It is obvious that  $G_t$  consists of a set of small cliques. Based on  $G_t$ , we define an aggregated graph  $G_A$  to summarize the cluster relationship among all the snapshots. In  $G_A$ , two objects form an edge if they are connected in any  $G_t$ s. Furthermore, we attach an inverted list for each edge, storing the associated timestamps in which the two objects are connected. An example of  $G_A$ , built on the trajectory database in Figure 1, is shown in Figure 5 (a). As long as two objects are clustered in any timestamp, they are connected in  $G_A$ . The object pair  $(o_1, o_2)$  appears in two clusters at timestamps 2 and 3 and is thus associated with an inverted list  $\{2,3\}$ .

We use star as the data structure to capture the pair relationships. To avoid duplication, as  $G_t$  is an undirected graph and an edge may appear in multiple stars, we enforce a global ordering among the objects and propose a concept named  $directed\ star$ .

**Definition 3** (Directed Star). Given a vertex with global id s, its directed star  $Sr_s$  is defined as the set of neighboring vertices with global id t > s. We call s the star ID.

With the global ordering, we can guarantee that each edge is contained in a unique star partition. Given the aggregated graph  $G_A$  in Figure 5 (a), we enumerate all the possible directed stars in Figure 5 (b). These stars are emitted from mappers to different reducers. The key is the star ID and the value is the neighbors in the star as well as the associated inverted lists. The reducer will then call the Apriori-based algorithm to enumerate all the valid GCMP patterns.

Before we introduce the Apriori enumerator, we are interested to examine the issue of global ordering on the moving

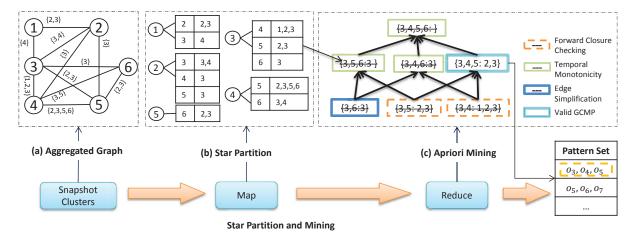


Figure 5: Star partition and mining. (a) Conceptual connection graph from Figure 1.(b) Five star partitions are generated (c) Apriori Mining with various pruning techniques.

objects. This is because assigning different IDs to the objects will result in different star partitioning results, which will eventually affect the workload balance among the mapreduce jobs. The job incurring performance bottleneck is often known as straggler [15, 16, 17]. In the context of star partitioning, a straggler refers to the job assigned with the maximum star partition. We use  $\Gamma$  to denote the size of a partition and  $\Gamma$  is set to the number of edges in a directed star<sup>1</sup>. It is straightforward that a star partitioning with small  $\Gamma$  is preferred. For example, Figure 6 gives two star partitioning results under different vertex ordering on the same graph. The top one has  $\Gamma=5$  while the bottom one has  $\Gamma=3$ . Obviously, the bottom one with smaller  $\Gamma$  is much more balanced.

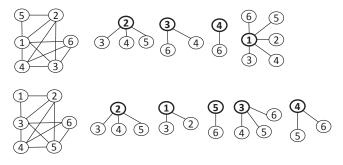


Figure 6: Examples of star partitioning with different vertex ordering.

Although it is very challenging to find the optimal vertex id ordering from the n! possibilities, we observe that a random order can actually achieve satisfactory performance based on the following theorem.

**Theorem 2.** Let  $\Gamma^*$  be the value derived from the optimal vertex ordering and  $\Gamma$  be value derived from a random vertex ordering. With probability 1 - 1/n, we have  $\Gamma = \Gamma^* + O(\sqrt{n \log n})$ .

*Proof.* In Appendix XXX. 
$$\Box$$

If  $G_A$  is a dense graph, we can get a tighter bound for  $(\Gamma - \Gamma^*)$ .

**Theorem 3.** Let d be the average degree in  $G_A$ . If  $d \ge \sqrt{12 \log n}$ , with high probability 1-1/n,  $\Gamma = \Gamma^* + O(\sqrt{d \log n})$ .

*Proof.* In Appendix XXXX. 
$$\Box$$

Hence, we can simply use object id to determine the vertex ordering in our implementation.

## **5.2** Apriori Enumerator

Intuitively, given a GCMP pattern with an object set  $\{o_1,o_2,\ldots,o_m\}$ , all the pairs of  $(o_i,o_j)$  with  $1\leq i< j\leq m$  must be connected in the associated temporal graphs  $\{G_t\}$ . This inspires us to leverage the classic Apriori algorithm to enumerate all the valid GCMP patterns starting from pairs of objects. However, we observe that the monotonicity property does not hold between an object set and its supersets.

**Example 1.** In this example, we show that if an object set is not a valid pattern, we cannot prune all its super sets. Consider two candidates  $P_1 = \{o_1, o_2 : 1, 2, 3, 6\}$  and  $P_2 = \{o_1, o_3 : 1, 2, 3, 7\}$ . Let L = 2, K = 3 and G = 2. Both candidates are not valid patterns because the constraint on L is not satisfied. However, when considering their object superset  $\{o_1, o_2, o_3\}$ , we can infer that their co-clustering timestamps are in (1, 2, 3). This is a valid pattern conforming to the constraints of L, K, G. Thus, we need a new type of monotonicity to facilitate pruning.

#### 5.2.1 Monotonicity

To ensure the monotonicity, we first introduce a procedure named  $star\ simplification$ , to reduce the number of edges as well as unnecessary timestamps in the inverted lists. For instance, if the size of the inverted list for an edge e is smaller than K, then the edge can be safely removed because the number of timestamps in which its supersets are clustered must also be smaller than K. To generalize the idea, we propose three concepts named  $maximal\ G$ -connected subsequence, decomposable sequence and sequence simplification.

**Definition 4** (Maximal G-connected Subsequence). A sequence T' is said to be a maximal G-connected subsequence

<sup>&</sup>lt;sup>1</sup>A star is essentially a tree structure and the number of nodes equals the number of edges minus one.

#### Algorithm 1 Line Sweep Mining

```
Require: \lambda_t = \{S_t, ..., S_{t+\eta-1}\}
 1: C \leftarrow \{\}
                                                       ▷ Candidate set
 2: for all clusters s in snapshot S_t do
 3:
         if |s| > M then
             C \leftarrow C \cup \{\langle s, t \rangle\}
 4:
 5:
         end if
 6: end for
 7: for all S_j \in \{S_{t+1}, \dots, S_{t+\eta-1}\} do
 8:
         N \leftarrow \{\}
 9:
         for all (c,s) \in C \times S_i do
10:
              c' \leftarrow \langle c.O \cap s.O, c.T \cup \{j\} \rangle
11:
              if c'.T is valid then
12:
                  output c'
              else if |c'.O| \geq M then
13:
14:
                  N \leftarrow N \cup \{c'\}
15:
              end if
16:
         end for
         for all c \in C do
17:
              if j - \max(c.T) \ge G then
18:
                  C \leftarrow C - \{c\}
19:
20:
                  output c, if c is a valid pattern
              end if
21:
22:
              if c's first segment is less than L then
23:
                  C \leftarrow C - \{c\}
24:
              end if
25:
         end for
         C \leftarrow C \cup N
26:
27: end for
28: output valid patterns in C
```

of T if (1) T' is the subsequence of T, i.e.,  $\exists i \leq j, T' = T(i,\ldots,j)$ , (2) T' is G-connected, and (3) there exists no other subsequence T'' of T such that T' is the subsequence of T'' and T'' is G-connected.

**Example 2.** Suppose G=2 and consider two sequences  $T_1=(1,2,4,5,6,9,10,11,13)$  and  $T_2=(1,2,4,5,6,8,9)$ .  $T_1$  has two maximal 2-connected subsequences:  $T_1^A=(1,2,4,5,6)$  and  $T_1^B=(9,10,11,13)$ . This is because the gap between  $T_1^A$  and  $T_1^B$  is 3 and it is impossible for the timestamps from  $T_1^A$  and  $T_1^B$  to form a new subsequence with  $G\leq 2$ . Since  $T_2$  is 2-connected,  $T_2$  has only one maximal 2-connected subsequence which is itself.

The maximal G-connected subsequence has the following two properties:

**Lemma 4.** Suppose  $\{T_1, T_2, \ldots, T_m\}$  is the set of all maximal G-connected subsequences of T, we have (1)  $T_i \cap T_j = \emptyset$  for  $i \neq j$  and (2)  $T_1 \cup T_2 \cup \ldots \cup T_m = T$ .

Proof. We assume  $T_i \cap T_j \neq \emptyset$ . Let  $T_i = (T_i[1], T_i[2], \dots, T_i[p])$  and  $T_j = (T_j[1], T_j[2], \dots, T_j[n])$ . Suppose T[x] is a timestamp occurring in both  $T_i$  and  $T_j$ . Let  $T[y] = \min\{T_i[1], T_j[1]\}$ , i.e., the minimum timestamp of  $T_i[1]$  and  $T_j[1]$  occurs at the y-th position of sequence T. Similarly, we assume  $T[z] = \max\{T_i[p], T_j[n]\}$ . Apparently, the two subsequences T[y:x] and T[x:z] are G-connected because  $T_i$  and  $T_j$  are both G-connected. Then, sequence  $(T_y, \dots, T_x, \dots, T_z)$ , the superset of  $T_i$  and  $T_j$ , is also G-connected. This contradicts with the assumptions that  $T_i$  and  $T_j$  are maximal G-connected subsequences.

## Algorithm 2 Temporal Replication and Parallel Mining

```
Require: list of \langle t, S_t \rangle pairs
 1: \eta \leftarrow (\lceil \frac{K}{L} \rceil - 1) * (G - 1) + K + L - 1
 2: —Map Phase-
 3: for all snapshots S_t do
         for all i \in 1...\eta - 1 do
 4:
 5:
             emit key-value pair \langle \max(t-i,0), S_t \rangle
 6:
         end for
 7: end for
 8: —Partition and Shuffle Phase-
 9: for all key-value pairs \langle t, S \rangle pair do
         group-by t and emit a key-value pair \langle t, \lambda_t \rangle, where
     \lambda_t = \{S_t, S_{t+1}, ... S_{t+\eta-1}\}
11: end for
12: —Reduce Phase—
13: for all key-value pairs \langle t, \lambda_t \rangle do
         call line sweep algorithm for partition \lambda_t
15: end for
```

To prove (2), we assume  $\cup_i T_i$  does not cover all the timestamps in T. Then, we can find a subsequence T' = T[x:x+t] such that  $T[x-1] \in T_a$   $(1 \le a \le m)$ ,  $T[x+t+1] \in T_b$   $(1 \le b \le m)$  and all the timestamps in T' is not included in any  $T_i$ . Let  $g' = \min\{T[x] - T[x-1], T[x+t+1] - T[x+t]\}$ . If  $g' \le G$ , then it is easy to infer that  $T_a$  or  $T_b$  is not a maximal G-connected subsequence because we can combine it with T[x] or T[x+t] to a form superset which is also G-connected. If g' > G, T' itself is a maximal G-connected subsequence which is missed in  $\cup T_i$ . Both cases lead to contradiction.

**Lemma 5.** If  $T_1$  is a subset of  $T_2$ , then for any maximal G-connected subsequence  $T'_1$  of  $T_1$ , we can find a maximal G-connected subsequence  $T'_2$  of  $T_2$  such that  $T'_1$  is a subset of  $T'_2$ .

Proof. Since  $T_1' \subseteq T_1 \subseteq T_2$ , we know  $T_1'$  is a G-connected subsequence of  $T_2$ . Based on Lemma 4, we can find a maximal G-connected subsequence of  $T_2$ , denoted by  $T_2'$ , such that  $T_1' \cap T_2' \neq \emptyset$ . If there exists a timestamp  $T_1'[x]$  such that  $T_1'[x] \notin T_2'$ , similar to the proof of case (1) in Lemma 4, we can obtain a contradiction. Thus, all the timestamps in  $T_1'$  must occur in  $T_2'$ .

**Definition 5** (Decomposable Sequence). T is decomposable if for any of its maximal G-connected subsequence T', we have (1) T' is L-consecutive; and (2)  $|T'| \ge K$ .

**Example 3.** Let L=2, K=4 and we follow the above example.  $T_1$  is not a decomposable sequence because one of its maximal 2-connected subsequence (i.e.,  $T_1^B$ ) is not 2-consecutive. In contrast,  $T_2$  is a decomposable sequence because the sequence itself is the maximal 2-connected subsequence, which is also 2-consecutive and with size no smaller than than 4.

**Definition 6** (Sequence Simplification). Given a sequence T, the simplification procedure  $sim(T) = g_{G,K} \cdot f_L(T)$  can be seen as a composite function with two steps:

- 1. f-step: remove segments of T that are not L-consecutive;
- 2. g-step: among the maximal G-connected subsequences of  $f_L(T)$ , remove those with size smaller than K.

**Example 4.** Take T = (1, 2, 4, 5, 6, 9, 10, 11, 13) as an example for sequence simplification. Let L = 2, K = 4 and G = 2. In the f-step, T is reduced to  $f_2(T) = (1, 2, 4, 5, 6, 9, 10, 11)$  equals to level are generated (Line 10). When two candidate sets G = 2 are joined, the new candidate becomes G = 2. In the G = 2 are joined, the new candidate becomes G = 2. The segment (13) is removed due to the constraint of G = 2 are joined, the new candidate becomes G = 2. In the G = 2 are joined, the new candidate becomes G = 2. The segment (13) is removed due to the constraint of G = 2 are joined, the new candidate becomes G = 2. In the G = 2 are joined, the new candidate becomes G = 2 are joined, the new candidate becomes G = 2 are joined, the new candidate becomes validity of the candidate, we calculate G = 2 validity of the candidate, we calculate G = 2 validity of the candidate set join. During each iteration (Lines 8-29), only candidates with object size for candidat

It is possible that the simplified sequence  $sim(T) = \emptyset$ . For example, Let T = (1, 2, 5, 6) and L = 3. All the segments will be removed in the f-step and the output is  $\emptyset$ . We define  $\emptyset$  to be not decomposable. We provide an important property of the sequence simplification process as follows:

**Lemma 6.** If sequence T is a superset of any decomposable sequence, then  $sim(T) \neq \emptyset$ .

*Proof.* It is obvious that sim(T) is a one-to-one function. Given an input sequence T, there is a unique sim(T). Let  $T_p$  be a decomposable subset of T and we prove the lemma by showing that sim(T) is a superset of  $T_p$ .

Suppose  $T_p$  can be decomposed into a set of maximal G-connected subsequences  $T_p^1, \ldots, T_p^m \ (m \geq 1)$ . Since  $T_p$  is a subset of T, all the  $T_p^i$  are also subsets of T. By definition, each  $T_p^i$  is L-consecutive. Thus, in the f-step of  $\mathbf{sim}(T)$ , none of  $T_p^i$  will be removed. In the g-step, based on Lemma 5, we know that each  $T_p^i$  has a superset in the maximal G-connected subsequences of  $f_L(T)$ . Since  $|T_p^i| \geq K$ , none of  $T_p^i$  will be removed in the g-step. Therefore, all the  $T_p^i$  will be retained after the simplification process and  $\mathbf{sim}(T) \neq \emptyset$ .  $\square$ 

With Lemma 6, we are ready to define the *monotonicity* based on the simplified sequences to facilitate the pruning in the Apriori algorithm.

**Theorem 7** (Monotonicity). Given a candidate pattern  $P = \{O : T\}$ , if  $sim(P.T) = \emptyset$ , then any pattern candidate P' with  $P.O \subseteq P'.O$  can be pruned.

Proof. We prove by contradiction. Suppose there exists a valid pattern  $P_2$  such that  $P_2.O \supseteq P.O$ . It is obvious that  $P_2.T \subseteq P.T$ . Based on the Definition 2, the following conditions hold: (1)  $P_2.T$  is G-connected. (2)  $|P_2.T| \ge K$  and (3)  $P_2.T$  is L-consecutive. Note that the entire  $P_2.T$  is G-connected. Thus,  $P_2.T$  itself is the only maximal G-connected subsequence. Based on conditions (1),(2),(3) and Definition 6,  $P_2.T$  is decomposable. Then, based on Lemma 6, we know  $sim(T) \ne \emptyset$  because  $P_2.T \subseteq P.T$  and  $P_2.T$  is decomposable. This leads to a contradiction with  $sim(P.T) = \emptyset$ . □

#### 5.2.2 Apriori Enumeration

We design an Apriori enumeration method to efficiently discover all the valid patterns in a star partition. The principle of Apriori algorithm is to construct a lattice structure and enumerate all the possible candidate sets in a bottom-up manner. Its merit lies in the monotonic property such that if a candidate set is not valid, then all its supersets can be pruned. Thus, it works well in practice in spite of the exponential search space.

Our customized Apriori Enumerator is presented in Algorithm 3. Initially, the edges (pairs of objects) in the star constitute the bottom level (Lines 2-6) and invalid candidates are excluded (Line 4). An indicator *level* is used

to control the object size for candidate set join. During each iteration (Lines 8-29), only candidates with object size equals to level are generated (Line 10). When two candidate sets  $c_1$  and  $c_2$  are joined, the new candidate becomes  $c' = \langle c_1.O \cup c_2.O, c_1.T \cap c_2.T \rangle$  (Lines 11). To check the validity of the candidate, we calculate  $\operatorname{sim}(c'.T)$ . If its simplified sequence is empty, c' is excluded from the next level (Line 12). This ensures that then all the candidates with  $P.O \supseteq c'.O$  are pruned. If a candidate cannot generate any new candidate, then it is directly reported as a valid closed pattern (Lines 16-20). To further improve the performance, we adopt the idea of forward closure [18, 19] and aggressively check if the union of all the current candidates form a valid pattern (Lines 22-27). If yes, we can early terminate the algorithm and output the results.

#### Algorithm 3 Apriori Enumerator

```
Require: Sr_s
 1: C \leftarrow \emptyset
 2: for all edges c = \langle o_i \cup o_j, T_{o_i} \cap T_{o_j} \rangle in Sr_s do
 3:
           if sim(T_{o_i} \cap T_{o_j}) \neq \emptyset then
 4:
               C \leftarrow C \cup \{c\}
 5:
           end if
 6: end for
 7: level \leftarrow 2
     while C \neq \emptyset do
 8:
 9:
           for all c_1 \in C do
10:
                for all c_2 \in C and |c_2.O \cup c_2.O| = \text{level do}
                     c' \leftarrow \langle c_1.O \cup c_2.O : (c_1.T \cap c_2.T) \rangle
11:
                     if sim(c'.T) \neq \emptyset then
12:
13:
                          C' \leftarrow C' \cup \{c'\}
                     end if
14:
15:
                end for
                if no c' is added to C' then
16:
17:
                     if c_1 is a valid pattern then
18:
                          output c_1
19:
                     end if
20:
                end if
21:
           end for
22:
           O_u \leftarrow \text{union of } c.O \text{ in } C
23:
           T_u \leftarrow \text{intersection of } c.T \text{ in } C
24:
           if \langle O_u, T_u \rangle is a valid pattern then
25:
                output \langle O_u, T_u \rangle
26:
                break:
27:
           C \leftarrow C' : C' \leftarrow \emptyset : \text{level} \leftarrow \text{level} + 1
29: end while
30: output C
```

**Example 5.** As shown in Figure 5(c), in the bottom level of the lattice structure, candidate  $\{3,6:3\}$  is pruned because its simplified sequence is empty. Thus, all the object sets containing  $\{3,6\}$  can be pruned. The remaining two candidates (i.e.,  $\{3,4:1,2,3\}$  and  $\{3,5:2,3\}$ ) derive a new  $\{3,4,5:2,3\}$  which is valid. By the forward closure checking, the algorithm can terminate and output  $\{3,4,5:2,3\}$  as the final closed pattern.

## **5.3** Put It Together

We summarize the workflow of SPARE in Figure 5 as follows. After the parallel clustering in each snapshot, for ease of presentation, we used an aggregated graph  $G_A$  to capture

the clustering relationship. However, in the implementation of the map phrase, there is no need to create  $G_A$  in advance. Instead, we simply need to emit the edges within a star partition to the same reducer. Each reducer is an Apriori Enumerator. When receiving a star  $Sr_i$ , the reducer creates initial candidate patterns. Specifically, for each  $o \in Sr_i$ , a candidate pattern  $\{o, i : e(o, i)\}$  is created. Then it enumerates all the valid patterns from the candidate patterns. The pseudocode of SPARE is presented in Algorithm 4.

Algorithm 4 Star Partition and ApRiori Enumerator

```
Require: list of \langle t, S_t \rangle pairs
 1: —Map phase-
 2: for all C \in S_t do
 3:
         for all o_1 \in C, o_2 \in C, o_1 < o_2 do
 4:
             emit a \langle o_1, o_2, \{t\} \rangle triplet
 5:
         end for
 6: end for
 7: —Partition and Shuffle phase—
 8: for all \langle o_1, o_2, \{t\} \rangle triplets do
         group-by o_1, emit \langle o_1, Sr_{o_1} \rangle
 9:
10: end for
11:
     -Reduce phase-
12: for all \langle o, Sr_o \rangle do
13:
         AprioriEnumerator(Sr_o)
14: end for
```

Compared with TPMP, the SPARE framework does not rely on snapshot replication to guarantee correctness. In addition, we can show that the patterns derived from a star partition are unique and there would not be duplicate patterns mined from different star partitions.

**Theorem 8** (Pattern Uniqueness). Let  $Sr_i$  and  $Sr_j$  ( $i \neq j$ ) be two star partitions. Let  $P_i$  (resp.  $P_j$ ) be the patterns discovered from  $Sr_i$  (resp.  $Sr_j$ ). Then,  $\forall p_i \in P_i, \forall p_j \in P_j$ , we have  $p_i.O \neq p_j.O$ .

*Proof.* We prove by contradiction. Suppose there exist  $p_i \in P_i$  and  $p_j \in P_j$  with the same object set. Note that the center vertex of the star is associated with the minimum id. Let  $o_i$  and  $o_j$  be the center vertices of the two partitions and we have  $o_i = o_j$ . However,  $P_i$  and  $P_j$  are different stars, meaning their center vertices are different (i.e.,  $o_i \neq o_j$ ), leading to a contradiction.

Theorem 8 implies that no mining efforts are wasted in discovering redundant patterns in the SPARE framework, which is superior to the TRPM baseline. Finally, we prove the correctness of the SPARE framework.

**Theorem 9.** The SPARE framework guarantees completeness and soundness.

*Proof.* See Appendix XXXX.  $\Box$ 

## 6. EXPERIMENTAL STUDY

In this section, we present our experimental findings on deploying our GCMP detectors to large-scaled real trajectories. All the experiments are carried out on our in-house cluster: Dianwei. The cluster includes 12 nodes, each of which is equipped with four quad-core 2.2GHz Intel processors, 32 GB memory and gigabit Ethernet. The cluster is installed with CentOS 5.5. operating system.

Environment Setup: We use Yarn<sup>2</sup> to manage our cluster. One node is dedicated as Yarn's master node, and each other node reserves one core and 2 GB memory for Yarn processes. We use Apache Spark 1.5.5 [20] as the MapReduce framework. Spark takes the remaining 11 nodes as the computing nodes. To fully utilize the computing power of the cluster, we assign each node to run five executors, each executor takes three cores and 5 GB memory. We use "yarn-cluster" mode for Spark which randomly picks one executor to act as the Application Master. Such a configuration allows us to run 162 tasks at the same time. We use HDFS as our storage engine with replicator factor of 1. The summary of the configuration is as in the following table:

Parameter	Value
Java Version	1.7.0
Spark Version	1.5.5
spark.driver.memory	2GB
spark.executor.cores	3
spark.executor.instances	54
spark.executor.memory	5GB
spark.master	yarn-cluster
spark.serializer	KryoSerializer

**Datasets**: We prepare three real datasets for experiments. The details of the datasets are as follows:

- Geolife <sup>3</sup>: this dataset collects 18,670 trajectories for passengers in Beijing over three years. The data are collected per around 5 seconds. Each data point records a trajectory ID and the latitude/longitude information.
- Shopping <sup>4</sup>: this dataset contains visitors trajectories in ATC shopping center in Osaka. The samples are taken per around 0.5 seconds. There are in total 13,183 trajectories. Each data point is a trajectory ID with in-door coordinates.
- Taxi: this dataset records 15,054 Singapore taxi trajectories over one month span. The sample rate is around 30 seconds. Each data point is the taxi plate with latitude/longitude information.

Preprocessing: We replace timestamps with global sequences for each dataset. The sequence number 0 is the earliest timestamp among all trajectories in a dataset. We use the sampling rate of each dataset as the tick of the sequence number and every data point is mapped to the nearest ticks. If several points mapped to the same tick, they are merged by averaging the location coordinates. For missing data within small intervals (i.e., sequence difference less than 10), we use linear interpolation to fill them. We then use DBSCAN ( $\epsilon = 5, minPt = 10$  for GeoLife and Shopping,  $\epsilon = 20, minPt = 10$  for Taxi) as the clustering algorithm for preprocessing. Note that both our TRPM and SPARE algorithms treat the preprocessing as a black box and other spatial clustering methods are also applicable. The clustered snapshots are stored in HDFS in  $\langle t, S_t \rangle$  pair, where t is the timestamp,  $S_t$  contains the clusters at snapshot t.

 $<sup>^2</sup> http://hadoop.apache.org/docs/current/hadoop-yarn/hadoop-yarn-site/YARN.html$ 

<sup>&</sup>lt;sup>3</sup>http://research.microsoft.com/en-us/projects/geolife/ <sup>4</sup>http://www.irc.atr.jp/crest2010\_HRI/ATC\_dataset/

After preprocessing, the statistics of the three datasets are presented in Table 5.

Attributes	ACTShopping	Geolife	SingTaxi
# objects	13,183	18,670	15,054
# average ts	3,114	2,924	19,667
# data points	41,052,242	54,594,696	296,075,837
# snapshots	16,931	10,699	44,364
# clusters	211,403	206,704	536,804
avg. cluster size	171	223	484

Table 5: Statistics of data set

**Parameters**: To systematically study the performance of our algorithms, we conduct experiments on various conditions. The variables to be tested and their value ranges are listed in Table 6. Default values are highlighted in bold.

Variables	Meaning	Values
M	min size of object set	5, 10, <b>15</b> , 20, 25
K	min duration	120, 150, <b>180</b> , 210, 240
L	min local duration	10, 20, <b>30</b> , 40,50
G	max gap	10, 15, <b>20</b> , 25, 30
N	number of executors	1, 14, 24, 34, 44, <b>54</b>

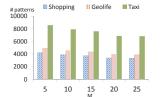
Table 6: Variables and their default values

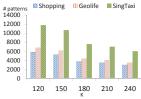
Number of patterns under different parameters: We first analyze the number of patterns exist in each dataset under different conditions. The results are presented in Figures 7. As expected, the number of patterns differs under in different scenarios. Larger M, L, K imply smaller number of patterns, because lesser patterns are able to meet stricter M, L, K constraints. In contrast, larger G implies larger number of patterns. This is because larger gaps relaxes the pattern constraint. Two interesting observations are made on L and G. First, as L increases from 10 to 20, the number of patterns drops quickly (50% less). Second, opposed to L's trend, as G reaches to 30 from 25, the number of patterns bursts (near 50% more). The distribution of patterns under G and L reveals that there are many companions in real life which are short and intermittent. With GCMP, we can discover these patterns by adjusting property L and Gs.

Algorithms: We implement TRPM, SPARE and SPARE-LB for comparison study. TRPM and SPARE are implement as described in Section 4 and 5. SPARE-LB extends SPARE by appending an additional load balance stage to the map phase. When the mappers complete, SPARE-LB collects the size of stars from all mappers. Then a best-fit strategy is applied for task allocation. In best-fit, tasks are assigned in decreasing order of their sizes, and the most costly unassigned task is allocated to the current mostly empty reducer. In SPARE-LB, we simply use the number of edges in stars as a cost estimation. The other part of SPARE-LB is identical with SPARE.

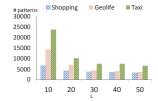
#### **6.1 Performance Comparison**

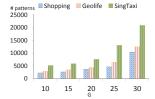
Since the both TRPM and SPARE utilizes pruning rules that related to the pattern parameters M,K,L,G. It is interesting to see their performances under different settings. We run the three algorithms using all three datasets and report their overall performances in Figures 8. In brief, all of the three algorithms are able to handle the large-scaled real datasets. However, SPARE algorithms are obviously





(a) Number of patterns vary M (b) Number of patterns vary K





(c) Number of patterns vary L (d) Number of patterns vary G

Figure 7: Number of patterns discovered from real datasets

more efficient than TRPM. In the case when G is large (i.e., G=30), TRMP takes near three hours for Taxi dataset, which is 15 times slower than SPARE algorithms. Besides, SPARE-LB is consistently more efficient than SPARE, with an average of 20% improvements. Another general observation is that all of the three algorithms run slower in the Taxi dataset as compared to other two datasets. This is because Taxi dataset contains the most number of temporal data points, which is around 7 times of Shopping dataset and 5 times of geolife dataset. In summary, SPARE outperforms TRMP in all cases. Next, we analyze the details of each experiments.

Vary M: Figures 8 (a),(e),(i) present the performance when M changes. As the figures show, SPARE based algorithms runs much faster than TRPM. We can see that SPARE speeds up TRPM 2.7 times in Shopping data, 3.1 times in Geolife data and 7 times in Taxi data. An interesting observation is that, the running times of all algorithms slightly decrease as M grows. This is because when M becomes bigger, smaller clusters or stars can be directly pruned, which brings in the efficiency.

**Vary** K: Figure 8 (b),(f),(j) presents the performances when K changes. There are two interesting findings. First, SPARE based algorithms and TRPM takes different trends as K increases. When K increases, SPARE and SPARE-LB tends to run faster while TRPM continuously slows down. For SPARE, the trends are resulted from more pruning powers brought by K. When K increases, more sequences can be pruned by the sequence simplification. Conversely, TRPM fails to utilize K for pruning. Moreover, as K increases,  $\eta$ in TRPM grows, indicating more replication of snapshots. This explains the low performance of TRPM. Second, when K is small (i.e, K=120), TRPM could outperform SPARE. This is because smaller K indicates small partition size in TRPM but restricted the pruning power in SPARE. As a result, TRPM wins 10% in Geolife dataset. However, by leveraging the load balancing, SPARE-LB is still faster than TRPM.

Vary L: Figures 8 (c)(g)(k) presents the performances when L changes. We can see that SPARE based algorithms are still superior than TRPM, where SPARE-LB outperforms TRPM near 10 times when L=10. An interesting

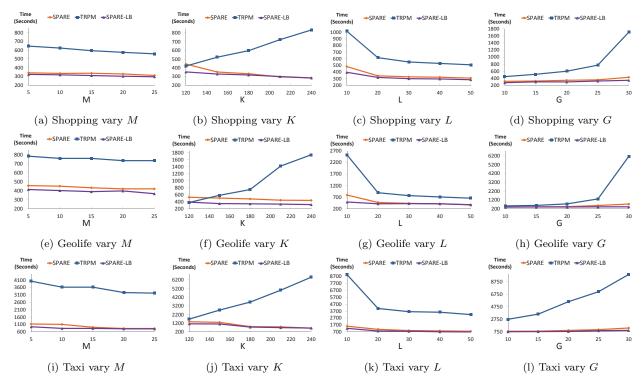


Figure 8: Performance of SPARE and TRPM on real datasets under different pattern parameters.

observation is that L provides good pruning power from 10 to 20 for both TRPM and SPARE based algorithms. The major reason is that the decrease of L invalidates many candidates (as shown in Figure 7 (c)), thus the prunings in both SPARE and TRPM become more significant. As L continues to increase, we can see that TRPM's performance gain is larger than SPARE based algorithms. This is because larger L indicates smaller  $\eta$ , which is more beneficial to TRPM.

**Vary** G: Figures 8 (d)(h)(l) presents the performances when G changes. Unlike other cases, when G increases, both TRPM and SPARE based algorithms run slower. The reason is that large G relaxes the constraint of a pattern, thus the pruning powers of TRPM and SPARE is more restricted. We observe that there is a burst in performance of TRPM when G reach to 30. The major reason is that when G becomes to 30, the number of valid patterns almost doubles as shown in Figure 7 (d). This indicate that during TRPM's line sweep, very few patterns can be pruned, making the candidate set grows exponentially. Similarly, SPARE algorithms are also affected by the increase of G. However we do not observe such a burst for SPARE. The reason is bifolded. First, SPARE can utilize K, L to retain the power of pruning. Second, SPARE leverages forward closure check to quickly output valid patterns and avoids to enumerating many candidates.

#### **6.2** Analysis of SPARE and SPARE-LB

As SPARE based algorithms are superior than TRPM, we further analyze several more aspects of SPARE namely, power of pruning, load balance and scalability.

#### 6.2.1 Power of sequence simplification

One of the core techniques used in SPARE is the  $sequence\ simplification$  (see Section 5.2.1). As shown in Algorithm 3, we use sim(T) to prune false candidates. To study the power of sequence simplification, we collect the total number of pairs that are pruned before apriori enumeration. The statistics are shown in Table 7 under default parameters. The result states that the  $sequence\ simplification$  is a very powerful pruning technique. It cuts off near 90% of the initial pairs, which significantly reduces the costs of later enumerations. This confirms the necessity and usefulness of design such a technique.

Data Set	Shopping	Geolife	Taxi
Before pruning	878,309	1,134,228	2,210,101
After pruning	76,672	123,410	270,921
Prune ratio	91.2%	89.1%	87.7%

Table 7: Pruning power of SPARE

#### 6.2.2 Load Balance

To study why SPARE-LB is more efficient, we analyze the running time of SPARE and SPARE-LB for each mapreduce stage. The detail anatomy is shown in Figure 9(a). We can see that on all three datasets, the reduce phase for both SPARE and SPARE-LB takes the majority time. The overall improvement of SPARE-LB is around 10-13% under the default settings. We observe that the map and shuffle time of SPARE and SPARE-LB are identical, where SPARE-LB spends a very small portion of extra time (4% of the total time) in applying the best-fit strategy. The time spent is worthwhile as in the reduce phase SPARE-LB saves around 20% of the time. However, since the star sizes in

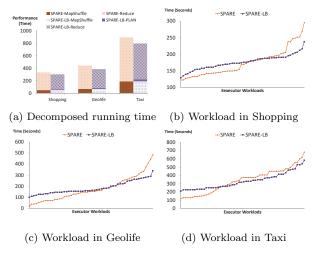


Figure 9: Load balance of SPARE and SPARE-LB

SPARE is almost identical (due to Theorem 2), the best-fit strategy does not win too significantly.

We then look at the workload distribution of SPARE and SPARE-LB on real datasets. We collect the statistics from executors and report their reduce times in Figure 9. The figure shows that SPARE-LB is able to provide a more balanced task allocation in all three cases. Since SPARE takes random assignment of stars, it is likely to assign many large stars to the same executor. As we can see the difference between stragglers in SPARE-LB and SPARE ranges from 60 seconds to 100 seconds. In general cases, SPARE-LB is recommended as it offers more efficiency while takes only a small extra time for planning.

#### 6.2.3 Scalability

We then study the scalability of SPARE-LB from two aspects. First, we fix the computing power and vary the size of dataset. We perform a random sample from the tree dataset and the results of SPARE-LB are shown in Figures 10. As the figures show, SPARE-LB grows almost linearly wrt |O| and |T|. This suggests a good scalability. Note that, as shown in Figure 3, a centralized algorithm runs more than a hundred times slower than SPARE for the same scale of data. This confirms the superiority of our parallel

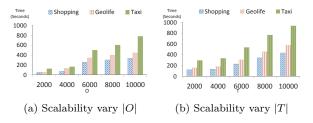


Figure 10: Scalability of SPARE-LB wrt. different data sizes

Second, we fix the work load and vary the number of executors. The result are presented in Figure 11. We can see that SPARE achieves good scalability under all three cases. For instance, for Taxi dataset, when the executors rises from 10 to 50, the performance improves 4.8 times which is almost linear to the increase of executors. Such pattern also

holds for the other two datasets. The reason for the good scalablity is that SPARE partitions the trajectories by objects and each partition is perfectly independent. Therefore, when the number of reducers N << |O|, SPARE can always speed up by adding more executors.

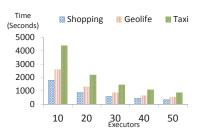


Figure 11: Scalability of SPARE-LB vary. N.

#### 7. CONCLUSION AND FUTURE WORK

#### 8. REFERENCES

- Y. Zheng, Y. Liu, J. Yuan, and X. Xie, "Urban computing with taxicabs," in *Proceedings of the 13th* international conference on Ubiquitous computing, pp. 89–98, ACM, 2011.
- [2] Z. Li, B. Ding, J. Han, R. Kays, and P. Nye, "Mining periodic behaviors for moving objects," in *Proceedings* of the 16th ACM SIGKDD international conference on Knowledge discovery and data mining, pp. 1099–1108, ACM, 2010.
- [3] J. Bao, Y. Zheng, D. Wilkie, and M. F. Mokbel, "A survey on recommendations in locationbased social networks. submitted to," *Geoinformatica*, 2013.
- [4] X. Li, Managing moving objects and their trajectories. PhD thesis, National University of Singapore, 2013.
- [5] J. Gudmundsson and M. van Kreveld, "Computing longest duration flocks in trajectory data," in Proceedings of the 14th annual ACM international symposium on Advances in geographic information systems, pp. 35–42, ACM, 2006.
- [6] Y. Wang, E.-P. Lim, and S.-Y. Hwang, "Efficient mining of group patterns from user movement data," *Data and Knowledge Engineering*, vol. 57, no. 3, pp. 240–282, 2006.
- [7] H. Jeung, M. L. Yiu, X. Zhou, C. S. Jensen, and H. T. Shen, "Discovery of convoys in trajectory databases," Proceedings of the VLDB Endowment, vol. 1, no. 1, pp. 1068–1080, 2008.
- [8] Z. Li, B. Ding, J. Han, and R. Kays, "Swarm: Mining relaxed temporal moving object clusters," *Proceedings* of the VLDB Endowment, vol. 3, no. 1-2, pp. 723–734, 2010.
- [9] Y. Li, J. Bailey, and L. Kulik, "Efficient mining of platoon patterns in trajectory databases," *Data and Knowledge Engineering*, 2015.
- [10] J. Gudmundsson, M. van Kreveld, and B. Speckmann, "Efficient detection of motion patterns in spatio-temporal data sets," in *Proceedings of the 12th annual ACM international workshop on Geographic information systems*, pp. 250–257, ACM, 2004.

- [11] Y. Zheng, "Trajectory data mining: an overview," ACM Transactions on Intelligent Systems and Technology (TIST), vol. 6, no. 3, p. 29, 2015.
- [12] D. Birant and A. Kut, "St-dbscan: An algorithm for clustering spatial-temporal data," *Data and Knowledge Engineering*, vol. 60, no. 1, pp. 208–221, 2007.
- [13] P. Laube, M. van Kreveld, and S. Imfeld, "Finding remodetecting relative motion patterns in geospatial lifelines," in *Developments in spatial data handling*, pp. 201–215, Springer, 2005.
- [14] D. H. Douglas and T. K. Peucker, "Algorithms for the reduction of the number of points required to represent a digitized line or its caricature," Cartographica: The International Journal for Geographic Information and Geovisualization, vol. 10, no. 2, pp. 112–122, 1973. doi:10.3138/FM57-6770-U75U-7727.
- [15] Y. Kwon, M. Balazinska, B. Howe, and J. Rolia, "Skewtune: mitigating skew in mapreduce applications," in *Proceedings of the 2012 ACM SIGMOD International Conference on Management of Data*, pp. 25–36, ACM, 2012.
- [16] R. S. Xin, J. Rosen, M. Zaharia, M. J. Franklin, S. Shenker, and I. Stoica, "Shark: Sql and rich analytics at scale," in *Proceedings of the 2013 ACM SIGMOD International Conference on Management of data*, pp. 13–24, ACM, 2013.
- [17] E. Coppa and I. Finocchi, "On data skewness, stragglers, and mapreduce progress indicators," in Proceedings of the Sixth ACM Symposium on Cloud Computing, pp. 139–152, ACM, 2015.
- [18] J. Wang, J. Han, and J. Pei, "Closet+: Searching for the best strategies for mining frequent closed itemsets," in *Proceedings of the ninth ACM SIGKDD* international conference on Knowledge discovery and data mining, pp. 236–245, ACM, 2003.
- [19] J. Pei, J. Han, R. Mao, et al., "Closet: An efficient algorithm for mining frequent closed itemsets.," in ACM SIGMOD workshop on research issues in data mining and knowledge discovery, vol. 4, pp. 21–30, 2000.
- [20] M. Zaharia, M. Chowdhury, T. Das, A. Dave, J. Ma, M. McCauley, M. J. Franklin, S. Shenker, and I. Stoica, "Resilient distributed datasets: A fault-tolerant abstraction for in-memory cluster computing," in *Proceedings of the 9th USENIX* conference on Networked Systems Design and Implementation, pp. 2–2, USENIX Association, 2012.

#### **APPENDIX**

## A. PROOFS OF THEOREMS

#### A.1 Proof of Theorem 2

*Proof.* We formalize optimization of  $\Gamma$  using a linear algebra model as follows: Let  $G_A$  be an aggregate graph, with a  $n \times n$  adjacent matrix J. A vertex order is in fact a permutation of J. Therefore, the adjacent matrices of any reordered graphs can be represented as  $PJP^T$  where  $P \in \mathbb{P}$  is a permutation

 $matrix^5$  with dimension n. Since in star partition, we assign each edge e(i,j) in  $G_A$  to the lower vertex, then the matrix  $B = \text{triu}(PJP^T)^6$  represents the assignment matrix wrt. P (i.e.,  $b_{i,j} = 1$  if vertex j is in star  $Sr_i$ ). Let vector  $\vec{b}$  be the  $one^7$  vector of size n. Let  $\vec{c} = B\vec{b}$ , then each  $c_i$  denotes the number of edges in star  $Sr_i$ . Thus,  $\Gamma$  can be represented as the infinity norm of  $B\vec{b}$ . Let  $\Gamma^*$  be the minimum  $\Gamma$  among all vertex orders.  $\Gamma^*$  can then be formulated as follows:

$$\Gamma^* = \min_{P \in \mathbb{P}} ||B\vec{b}||_{\infty} \text{ ,where } ||B\vec{b}||_{\infty} = \max_{1 \le j \le n} (c_j)$$
 (1)

Let B\* be the assignment matrix wrt the optimal vertex order. Since we have a star for each object, by the degreesum formula and pigeon-hole theorem,  $\Gamma^* = ||B^*\vec{b}||_{\infty} \geq d/2$ . Next, given a numbering P, let  $e_{i,j}$  be an entry in  $PAP^T$ . Since edges in graph G are independent, then  $e_{i,j}$ s are independent. Moreover, let  $d_i$  denote the degree of vertex i, then  $E[d_i] = E[\Sigma_{1 \leq j \leq n} e_{i,j}] = d$ . This is because renumbering the vertexes does not affect the average degree. Since  $B = \text{triu}(PAP^T)$ , entries in B can be written as:

$$b_{i,j} = \begin{cases} e_{i,j}, i > j \\ 0, otherwise \end{cases}$$

There are two observations made. First, since  $e_{i,j}$ s are independent,  $b_{i,j}$ s are independent. Second, since i > j and  $e_{i,j}$ s are independent.  $E[b_{i,j}] = E[e_{i,j}]E[i > j] = E[e_{i,j}]/2$ .

By definition,  $c_i = \sum_{1 \leq j \leq n} b_{i,j}$ , is a sum of n independent 0-1 variables. Taking expectation on both sides, we get:  $E[c_i] = E[\sum_{1 \leq j \leq n} b_{i,j}] = E[\sum_{1 \leq j \leq n} e_{i,j}]/2 = d/2$ . Let  $\mu = E[c_i] = d/2$ ,  $t = \sqrt{n \log n}$ , by Hoeffding's Inequality, the following holds:

$$Pr(c_i \ge \mu + t) \le \exp(\frac{-2t^2}{n})$$
$$= \exp(-2\log n) = n^{-2}$$

The first step is due to the fact that all  $b_{i,j}$  are bounded in the range of [0,1]. Next, since the event  $(\max_{1 \le j \le n} (c_j) \ge \mu + t)$  can be viewed as  $\cup_{c_i} (c_i \ge \mu + t)$ , by Union Bound, we achieve the following:

$$\begin{split} Pr(\Gamma \geq \mu + t) &= Pr(\max_{1 \leq j \leq n}(c_j) \geq \mu + t) \\ &= Pr(\cup_{c_i}(c_i \geq \mu + t)) \\ &\leq \Sigma_{1 \leq i \leq n} Pr(c_i \geq \mu + t) \\ &= n^{-1} = 1/n \end{split}$$

Substitute back t and  $\mu$ , we achieve the following concise form:

$$Pr(\Gamma \ge (d/2 + \sqrt{n \log n})) \le 1/n$$

This indicates that, the probability of  $(\Gamma - d/2)$  being less than or equal to  $O(\sqrt{n\log n})$  is (1-1/n). With the fact that  $\Gamma^* \geq d/2$ , we conclude that with probability greater than (1-1/n), the difference between  $\Gamma$  and  $\Gamma^*$  is less than  $O(\sqrt{n\log n})$ . When the aggregated graph is dense (i.e.,  $d \geq \sqrt{12\log n}$ ), we may use the Chernoff Bound instead of Hoeffding's Inequality to derive a tighter bound of  $O(\sqrt{\log n})$  with the similar reasoning.

 $<sup>^{5}\</sup>mathrm{an}$  identity matrix with rows shuffled

<sup>&</sup>lt;sup>6</sup>triu is the upper triangle part of a matrix

<sup>&</sup>lt;sup>7</sup>every element in  $\vec{b}$  is 1

## A.2 Proof of Theorem 9

*Proof.* For soundness, let P be a pattern enumerated by SPARE. Since the enumerate algorithm only reduces the time sequences, for any two objects  $o_1, o_2 \in P.O$ , the edge  $e(o_1, o_2)$  is a superset of P.T. By the definition of star,  $\forall t \in T, C_t(o_1) = C_t(o_2)$ . As T is a valid sequence, by the definition of GCMP, P is a true pattern. For completeness, let P is a true pattern. Let s be the object with smallest ID in P.O. We prove that P must be output by Algorithm 3 with input  $Sr_s$ . First, based on the definition of star, every object in P.O appears in  $Sr_s$ . Since P.T is decomposable, then  $\forall O' \subseteq O$ , the time sequence of O' is a super set of a decomposable sequence. This indicates that  $O^\prime$  would not be eliminated by any sim operations in Algorithm 3. Next, we prove at every iteration level  $\leq |P.O|$ ,  $P.O \subset O_u$ , where  $O_u$ is the forward closure. We prove by induction. When level = 2, it obviously holds. If  $P.O \subset O_u$  at level=i, then any subset of P.O with size i are in the candidate set. In leveli+1, these subsets are able to grow to a bigger subset (in last iteration, they grow to P.O). This suggests that no subsets are removed by Lines 16-30. Then,  $P.O \subset U_{i+1}$  holds. In summary, P.O does not pruned by simplification, monotonicity and forward closure, therefore P must be returned by SPARE.

14